SEQUENCE LISTING

<110> Wang, Yi
Mueller, John P.
Matis, Louis A.
<120> Chimeric Protiens and uses thereof for the Diagnosis, Prevention, and Treatment of Diabetes
<130> ALX-156 PCT
<140> Not Yet Assigned
<141> 1998-12-18
<150> 60/068,648
<151> 1997-12-22
<160> 37
<170> PatentIn Ver. 2.0
<210> 1
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Arg Glu Ala Glu Asp Leu Asn Met Tyr Ala Met Met Ile Ala Arg Phe
        35                  40                  45
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
    50                  55                  60
Leu Ile Ala Phe Thr Ser Glu Lys Cys Leu Glu Leu Ala Glu Tyr Leu
65                  70                  75                  80
Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp Gly
                85                  90                  95
Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser Leu
            100                 105                 110
Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg Leu Ser Lys Val
        115                 120                 125
Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly Thr Thr Met Val
    130                 135                 140
Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn His His His His His His
145                 150                 155                 160
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Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
            20                  25                  30
Arg Glu Ala Glu Asp Leu Met Asn Ile Leu Leu Gln Tyr Val Val Lys
        35                  40                  45
Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe
    50                  55                  60
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Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala
 65                  70                  75                  80
Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu
                85                  90                  95
Ala Glu Tyr Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met
            100                 105                 110
Val Phe Asp Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile
        115                 120                 125
Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu Arg Met Ser Arg
    130                 135                 140
Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met Met Glu Tyr Gly
145                 150                 155                 160
Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys Val Asn His His
                165                 170                 175
His His His His
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      Protein
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Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
            20                  25                  30
Arg Glu Ala Glu Asp Leu Met Asn Ile Leu Leu Gln Tyr Val Val Lys
        35                  40                  45
Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe
    50                  55                  60
Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala
 65                  70                  75                  80
Phe Thr Ser Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu
                85                  90                  95
Ala Glu Tyr Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met
            100                 105                 110
Val Phe Asp Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile
        115                 120                 125
Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn His His His His His His
    130                 135                 140
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      Protein
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Met Phe Val Asn Gln His Leu Cys Gly Ser His Leu Val Glu Ala Leu
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Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
            20                  25                  30
Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
        35                  40                  45
Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
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    50                  55                  60
Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
 65                  70                  75                  80
Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
                85                  90                  95
Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
            100                 105                 110
Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
        115                 120                 125
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
    130                 135                 140
Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
145                 150                 155                 160
Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile His
                165                 170                 175
His His His His His
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SUB A1

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<223> Description of Artificial Sequence:IG5 Fusion
      Protein
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Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
            20                  25                  30
Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
        35                  40                  45
Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
    50                  55                  60
Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
 65                  70                  75                  80
Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
                85                  90                  95
Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
            100                 105                 110
Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
        115                 120                 125
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
    130                 135                 140
Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
145                 150                 155                 160
Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly
                165                 170                 175
Gly Gly Tyr Ile Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu
            180                 185                 190
Arg Met Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met
        195                 200                 205
Met Glu Tyr Gly Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys
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Val Asn His His His His His His
225                 230
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<212> PRT
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<223> Description of Artificial Sequence:IG6 Fusion Protein
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 1               5                  10                  15
Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
            20                  25                  30
Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
        35                  40                  45
Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
    50                  55                  60
Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
65                  70                  75                  80
Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
                85                  90                  95
Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
            100                 105                 110
Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
        115                 120                 125
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
    130                 135                 140
Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
145                 150                 155                 160
Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly
                165                 170                 175
Gly Gly Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile Ala Thr Gln
            180                 185                 190
Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met Val Trp Glu
        195                 200                 205
Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val Glu Asp Gly
    210                 215                 220
Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ala Ser Leu Tyr
225                 230                 235                 240
His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp Cys Glu Asp
                245                 250                 255
Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr Gln Glu Thr
            260                 265                 270
Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala Glu Gly Thr
        275                 280                 285
Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys Val Asn Lys
    290                 295                 300
Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys Ser Asp Gly
305                 310                 315                 320
Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val Leu Asn Arg
                325                 330                 335
Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr Leu Glu His
            340                 345                 350
Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp Gln Phe Glu
        355                 360                 365
Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile Leu Lys Ala
    370                 375                 380
Leu Pro Gln His His His His His His
385                 390
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<210> 7

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Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
20 25 30
Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
35 40 45
Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
50 55 60
Lys Arg Gly Thr Asn Met Phe Thr Tyr Glu Ile Ala Pro Val Phe Val
65 70 75 80
Leu Leu Glu Tyr Val Thr Leu Lys Lys Met Arg Glu Ile Ile Gly Trp
85 90 95
Pro Gly Gly Ser Gly Asp Gly Gly Gly Met Asn Ile Leu Leu Gln Tyr
100 105 110
Val Val Lys Ser Phe Asp Asn Met Tyr Ala Met Met Ile Ala Arg Phe
115 120 125
Lys Met Phe Pro Glu Val Lys Glu Lys Gly Met Ala Ala Leu Pro Arg
130 135 140
Leu Gly Gly Gly Ile Ala Phe Thr Ser Glu His Ser His Phe Ser Leu
145 150 155 160
Lys Lys Gly Ala Ala Ala Leu Gly Ile Gly Thr Asp Ser Val Ile Gly
165 170 175
Gly Gly Tyr Ile Pro Pro Ser Leu Arg Thr Leu Glu Asp Asn Glu Glu
180 185 190
Arg Met Ser Arg Leu Ser Lys Val Ala Pro Val Ile Lys Ala Arg Met
195 200 205
Met Glu Tyr Gly Thr Thr Met Val Ser Tyr Gln Pro Leu Gly Asp Lys
210 215 220
Val Asn Gly Gly Gly Ile Glu His Asp Pro Arg Met Pro Ala Tyr Ile
225 230 235 240
Ala Thr Gln Gly Pro Leu Ser His Thr Ile Ala Asp Phe Trp Gln Met
245 250 255
Val Trp Glu Ser Gly Cys Thr Val Ile Val Met Leu Thr Pro Leu Val
260 265 270
Glu Asp Gly Val Lys Gln Cys Asp Arg Tyr Trp Pro Asp Glu Gly Ala
275 280 285
Ser Leu Tyr His Val Tyr Glu Val Asn Leu Val Ser Glu His Ile Trp
290 295 300
Cys Glu Asp Phe Leu Val Arg Ser Phe Tyr Leu Lys Asn Val Gln Thr
305 310 315 320
Gln Glu Thr Arg Thr Leu Thr Gln Phe His Phe Leu Ser Trp Pro Ala
325 330 335
Glu Gly Thr Pro Ala Ser Thr Arg Pro Leu Leu Asp Phe Arg Arg Lys
340 345 350
Val Asn Lys Cys Tyr Arg Gly Arg Ser Cys Pro Ile Ile Val His Cys
355 360 365
Ser Asp Gly Ala Gly Arg Thr Gly Thr Tyr Ile Leu Ile Asp Met Val
370 375 380
Leu Asn Arg Met Ala Lys Gly Val Lys Glu Ile Asp Ile Ala Ala Thr
385 390 395 400

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Leu Glu His Val Arg Asp Gln Arg Pro Gly Leu Val Arg Ser Lys Asp
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Gln Phe Glu Phe Ala Leu Thr Ala Val Ala Glu Glu Val Asn Ala Ile
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Leu Lys Ala Leu Pro Gln His His His His His His
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Tyr Leu Val Cys Gly Glu Arg Gly Phe Phe Tyr Thr Pro Lys Thr Arg
            20                  25                  30
Arg Glu Ala Glu Asp Leu Gln Val Gly Gln Val Glu Leu Gly Gly Gly
        35                  40                  45
Pro Gly Ala Gly Ser Leu Gln Pro Leu Ala Leu Glu Gly Ser Leu Gln
    50                  55                  60
Lys Arg Gly Met Asn Ile Leu Leu Gln Tyr Val Val Lys Ser Phe Asp
65                  70                  75                  80
Asn Met Tyr Ala Met Met Ile Ala Arg Phe Lys Met Phe Pro Glu Val
                85                  90                  95
Lys Glu Lys Gly Met Ala Ala Leu Pro Arg Leu Ile Ala Phe Thr Ser
            100                 105                 110
Glu His Ser His Phe Ser Leu Lys Lys Cys Leu Glu Leu Ala Glu Tyr
        115                 120                 125
Leu Tyr Asn Ile Ile Lys Asn Arg Glu Gly Tyr Glu Met Val Phe Asp
    130                 135                 140
Gly Lys Pro Gln His Thr Asn Val Cys Phe Trp Tyr Ile Pro Pro Ser
145                 150                 155                 160
Leu Arg Thr Leu Glu Asp Asn His His His His His His
                165                 170
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tgcggtgaac gcggcttttt ctacaccccg aaaacccgtc gtgaagcgga agatctgaac 120
atgtatgcca tgatgatcg 139
<210> 12
<211> 143
<212> DNA
<213> Artificial Sequence
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<400> 12
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caatcagacg cggcagcgcg gccatacctt tttctttaac ttccgggaac attttaaagc 120
gcgcgatcat catggcatac atg 143
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<210> 13
<211> 138
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<223> Description of Artificial Sequence:prIG3 primer
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taccaacgtt tgcttttggt acatcccgcc gagcctgcgt accctggaag ataacgaaga 120
acgcatgagc cgtctgtc 138
<210> 14
<211> 132
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<223> Description of Artificial Sequence:prIG4 primer
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catggtggtg ccatattcca tcatgcgcgc tttaataacc ggggcaactt tagacagacg 120
gctcatgcgt tc 132
<210> 15
<211> 18
<212> DNA
<213> Artificial Sequence
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<223> Description of Artificial Sequence:prIG5 primer
<400> 15
catatgttcg ttaaccag 18
<210> 16
<211> 18
<212> DNA
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<223> Description of Artificial Sequence:prIG6 primer
<400> 16
ggatccttaa tggtgatg 18
<210> 17
<211> 492
<212> DNA
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Protein coding sequence
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atgtatgcca tgatgatcgc gcgctttaaa atgttcccgg aagttaaaga aaaaggtatg 180
gccgcgctgc cgcgtctgat tgcctttacc tctgaaaaat gtctggaact ggcggaatat 240
ctgtacaaca tcattaaaaa ccgcgaaggc tatgaaatgg ttttcgatgg taaaccgcag 300
cataccaacg tttgcttttg gtacatcccg ccgagcctgc gtaccctgga agataacgaa 360
gaacgcatga gccgtctgtc taaagttgcc ccggttatta aagcgcgcat gatggaatat 420
ggcaccacca tggttagcta ccagccgctg ggtgataaag ttaaccacca tcaccatcac 480
cattaaggat cc 492
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gatg 64
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<211> 78
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taaaggcaat cagacgcg 78
<210> 20
<211> 27
<212> DNA
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<210> 21
<211> 552
<212> DNA
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<223> Description of Artificial Sequence:IG2 Fusion
Protein coding sequence
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aacattctgc tgcagtatgt tgttaaaagc ttcgataaca tgtatgccat gatgatcgcg 180
cgctttaaaa tgttcccgga agttaaagaa aaaggtatgg ccgcgctgcc gcgtctgatt 240
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cattaaggat cc 552

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<210> 23
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<223> Description of Artificial Sequence:IG3 Fusion
Protein coding sequence
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cgctttaaaa tgttcccgga agttaaagaa aaaggtatgg ccgcgctgcc gcgtctgatt 240
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<210> 24
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Protein coding sequence
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<400> 25
catatgttcg ttaaccagca tctg 24
<210> 26
<211> 69
<212> DNA
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<223> Description of Artificial Sequence:prIG15 primer
<400> 26

gctgcctgca ccagggcccc cgcccagctc cacctgcccc acctgcagat cttccgcttc 60
acgacgggt 69

<210> 27
<211> 66
<212> DNA
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<400> 27
agtgccacgc ttctgcaggg acccctccag ggccaagggc tgcaggctgc ctgcaccagg 60
gccccc 66
<210> 28
<211> 69
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ttccaaaagc acaaatactg gagcaatttc ataggtgaac atgttagtgc cacgcttctg 60
cagggaccc 69
<210> 29
<211> 69
<212> DNA
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<223> Description of Artificial Sequence:prIG18 primer
<400> 29
ccctggccag ccaatgattt ctctcatttt ctttagtgtg acatattcca aaagcacaaa 60
tactggagc 69
<210> 30
<211> 69
<212> DNA
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<223> Description of Artificial Sequence:prIG19 primer
<400> 30
agagaaatca ttggctggcc agggggctct ggcgatggag gcggtatgaa cattctgctg 60
cagtatgtt 69
<210> 31
<211> 68
<212> DNA
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<223> Description of Artificial Sequence:prIG20 primer
<400> 31
cagagaaaaa tggctatgtt cagaggtaaa ggcaataccg cctcccagac gcggcagcgc 60
ggccatac 68
<210> 32
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<223> Description of Artificial Sequence:prIG21 primer
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<210> 34
<211> 24
<212> DNA
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<223> Description of Artificial Sequence:prIG23 primer
<400> 34
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sub A17

<210> 35
<211> 708
<212> DNA
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<223> Description of Artificial Sequence:IG5 Fusion
Protein coding sequence
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gtggggcagg tggagctggg cgggggccct ggtgcaggca gcctgcagcc cttggccctg 180
gaggggtccc tgcagaagcg tggcactaac atgttcacct atgaaattgc tccagtattt 240
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tctggcgatg gaggcggtat gaacattctg ctgcagtatg ttgttaaaag cttcgataac 360
atgtatgcca tgatgatcgc gcgctttaaa atgttcccgg aagttaaaga aaaaggtatg 420
gccgcgctgc cgcgtctggg aggcggtatt gcctttacct ctgaacatag ccatttttct 480
ctgaaaaaag gagctgcagc cttagggatt ggaacagaca gcgtgattgg aggcggttac 540
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gttgccccgg ttattaaagc gcgcatgatg gaatatggca ccaccatggt tagctaccag 660
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:IG6 Fusion
Protein coding sequence
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gaggggtccc tgcagaagcg tggcactaac atgttcacct atgaaattgc tccagtattt 240
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gcagacttct ggcagatggt gtgggagagc ggctgcaccg tcatcgtcat gctgaccccg 660
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<210> 37
<211> 1344
<212> DNA
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:IG7 Fusion
Protein coding sequence

SUB A2

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catcaccatc accattaagg atcc 1344